WHAT IS CLAIMED IS:

1. A method for high information resolution of at least one analyte in a sample comprising the steps of:

a) exposing the analyte to at least two different selectivity conditions, each selectivity condition defined by the combination of an adsorbent and an eluant, to allow retention of the analyte by the adsorbent; and

b) detecting retained analyte under the different selectivity conditions by desorption spectrometry;

whereby detection of retained analyte under the different selectivity conditions provides a high information resolution of the analyte.

2. The method of claim 1 wherein each different selectivity condition is defined at a different predetermined, addressable location for parallel processing.

3. The method of claim 1 comprising the steps of:

i) exposing the analyte to a first selectivity condition at a defined location to allow retention of the analyte by the adsorbent;

ii) detecting retained analyte under the first selectivity condition by desorption spectrometry;

iii) washing the adsorbent under a second, different selectivity condition at the defined location to allow retention of the analyte to the adsorbent; and

iv) detecting retained analyte under the second selectivity condition by desorption spectrometry.

4. The method of claim 1 wherein the analyte is an organic biomolecule.

5. The method of claim 1 wherein the analyte is a virus or a cell.

6. The method of claim 1 wherein the adsorbent comprises an anion, a cation, a hydrophobic interaction adsorbent, a polypeptide, a nucleic acid, a carbohydrate, a lectin, a dye, a reducing agent, a hydrocarbon or a combination thereof.

7. The method of claim 1 wherein the different selectivity conditions comprise different binding conditions.

8. The method of claim 1 wherein the different selectivity conditions comprise different elution conditions.

9. The method of claim 1 wherein the step of detecting comprises detecting the mass of the analyte by laser desorption mass spectrometry.

10. The method of claim 1 wherein selectivity conditions are selected to optimize retention of analyte by an adsorbent.

11. The method of claim 1 wherein the adsorbent is attached to a substrate comprising glass, ceramic, a magnetic material, an organic polymer, a conducting polymer, a native biopolymer, a metal, a metal coated with an organic polymer or a combination thereof.

12. The method of claim 1 wherein the adsorbent is in the form of a microemulsion, a latex, a layer or a bead.

13. The method of claim 2 wherein the locations are arranged in a line, an orthogonal array or a circle.

14. The method of claim 2 wherein the adsorbents are located on a substrate at different locations before the analytes are exposed to the selectivity conditions.

15. The method of claim 2 wherein the adsorbents are located on a substrate at different locations after the analytes are exposed to the selectivity conditions.

16. The method of claim 2 wherein at least one analyte is more than one analyte.

17. The method of claim 2 wherein the plurality of selectivity conditions are defined by at different adsorbents and the same eluant.

18. The method of claim 2 further comprising the step of providing a substrate comprising adsorbents at addressable locations, each adsorbent being an adsorbent from a selectivity condition identified to retain the analyte.

19. The method of claim 2 comprising the steps of:

a) exposing a sample comprising the analytes to a first selectivity condition to allow retention of analytes by a first adsorbent and to create un-retained sample;

b) collecting the un-retained sample comprising analytes, exposing the un-retained sample to a second selectivity condition to allow retention of analytes by a second adsorbent and to create a second un-retained sample; and

c) detecting retained analyte under the different selectivity conditions by desorption spectrometry.

20. The method of claim 4 wherein the organic biomolecule is an enzyme, an immunoglobulin, a cell surface receptor or an intracellular receptor.

21. The method of claim 8 wherein the elution conditions differ according to pH, buffering capacity, ionic strength, a water structure characteristic, detergent type, detergent strength, hydrophobicity or dielectric constant.

22. The method of claim 18 wherein the plurality of selectivity conditions are defined by the same eluant.

23. The method of claim 19 further comprising the steps of collecting the second un-retained sample.

24. A substrate for desorption spectrometry comprising an adsorbent whose binding characteristics vary in a gradient along one or more linear axes.

25. A method for preparative purification of an analyte from an impure sample comprising the steps of:

a) exposing the sample to a substrate under a plurality of different selectivity conditions; detecting retained analyte under the different selectivity conditions by desorption spectrometry; and identifying selectivity conditions under which the analyte is retained;

b) purifying the analyte by repeating, for a plurality of different identified selectivity conditions, a sequence of steps comprising:

i) exposing the sample to an adsorbent under the identified selectivity condition to allow retention of the analyte by the adsorbent;

ii) separating the analyte from an impurity that is not retained by the substrate; and

iii) collecting the analyte from the adsorbent;

whereby the analyte is purified.

26. A method for selecting identity candidates for an analyte protein comprising the steps of:

a) determining a value set specifying match parameters for at least a first and second physico-chemical characteristic of a protein analyte in a sample by i) exposing the analyte to a plurality of different selectivity conditions, wherein adsorption of the protein analyte to the substrate is mediated by a basis of attraction that identifies a physico-chemical characteristic of the protein analyte; and ii) detecting retained analyte under the different selectivity conditions by desorption spectrometry; and

b) performing, in a programmable digital computer, the steps of:

i) accessing a database comprising, for each member of a set of reference polypeptides, a value set specifying at least a first and second physico-chemical characteristic of the reference polypeptides;

ii) accessing the value set specifying the physico-chemical characteristics of the protein analyte;

iii) sorting from the database, reference polypeptides having value sets within the match parameters;

whereby the sorted reference polypeptides provide identity candidates for the protein analyte and unsorted reference polypeptides provide non-identity candidates for the protein analyte.

27. The method of claim 26 wherein at least one physico-chemical characteristic is molecular mass.

28. The method of claim 26 wherein the database comprises, for each member of the set of reference polypeptides, an amino acid sequence of the polypeptide or a nucleotide sequence encoding the amino acid sequence of the polypeptide, and wherein the performing step further comprises providing code that derives the physico-chemical characteristics of a reference polypeptide from the amino acid sequence of the polypeptide.

29. The method of claim 27 wherein at least one of the physico-chemical characteristics is hydrophobicity, pI, number of coordinate covalent bonding residues or charge.

30. A method of detecting an enzyme in a sample comprising the steps of:

a) providing a solid phase comprising an adsorbent and an enzyme substrate bound to the adsorbent, wherein the activity of the enzyme on the enzyme substrate produces a product having a characteristic molecular mass;

b) exposing the substrate to the sample; and

c) detecting the product by desorption spectrometry;

whereby detecting the product provides a detection of the enzyme.

31. The method of claim 30 for determining the amount of the enzyme wherein the step of detecting comprises detecting an amount of the product, and comparing the detected amount to a standard that relates the detected amount to an amount of the enzyme in the sample.